CLAIMS

1. A method for assessing immune response profiles of animal populations comprising in operable combination the steps of:

a) obtaining:

i) dendritic cells and CD4+ T-cells from an individual within said animal population,

ii) and at least one protein sequence of interest;

b) producing peptides comprising fragments of said protein sequence of interest, such that the entire protein sequence of interest is encompassed in said fragments;

c) differentiating said dendritic cells to produce differentiated dendritic cells;

d) exposing said peptides to said CD4+ T-cells and said differentiated dendritic cells;

e) assessing the proliferation response of said CD4+ T-cells to each peptide; and

f) determining the stimulation index of said proliferation response of said CD4+ T-cells to each of said peptides;

g) repeating steps a) to f) for at least one additional individual;

h) comparing the results for said individual and said at least one additional individual, such that the immune response of multiple individuals is provided.

2. The method of Claim 1, wherein a stimulation index of at least about 1.5 is recorded as positive.

3. The method of Claim 1, wherein said animal population is a human population.

4. The method of Claim 3, wherein the structure values of the responses observed for individuals within the population are determined.

5. The method of Claim 4, wherein said steps a) through h) are repeated using at least one additional protein of interest.

6. The method of Claim 5, wherein said structure values of the responses for said protein of interest and said at least one additional protein of interest are used to rank the relative immunogenicity of said protein of interest and said at least one additional protein of interest.

7. The method of Claim 6, wherein the protein having the lower structure value is ranked as being less immunogenic than a protein having a higher structure value.

8. The method of Claim 5, wherein said at least one additional protein of interest comprises said protein of interest that has been modified to produce a modified protein of interest.

9. The method of Claim 8, wherein said modified protein of interest is selected from the group consisting of hypoimmunogenic proteins and hyperimmunogenic proteins.

10. The method of Claim 8, wherein said modified protein of interest is produced by substituting at least one amino acid in said at least one additional protein of interest to produce a variant protein of interest.

11. The method of Claim 6, wherein said protein of interest and said at least one additional protein of interest are selected from the group of proteins consisting of enzymes, antibodies, soluble receptors, fusion proteins, structural proteins, binding proteins, and hormones.

12. The method of Claim 9, wherein said enzyme is selected from the group consisting of proteases, subtilisins, cytokines, lipases, cellulases, amylases, oxidases, isomerases, kinases, phosphatases, lactamases, and reductases.

13. The method of Claim 1, further comprising a validation assay comprising a peripheral blood mononuclear cell response assessment.

14. A method for ranking the relative immunogenicity of a first protein and at least one additional protein, comprising the following steps in operable order:

(a) preparing a first pepset from said first protein and preparing at least one additional pepset from each of said additional proteins,

(b) obtaining solutions comprising dendritic cells and a solutions of naïve CD4+ and/or CD8+ T-cells, wherein each of said solutions is obtained from a first human blood source;

(c) obtaining solutions comprising dendritic cells and a solutions of naïve CD4+ and/or CD8+ T-cells, wherein each of said solutions is obtained from at least one additional human blood source;

(d) differentiating said dendritic cells from each of the human blood sources of steps (b) and (c), to produce solutions of differentiated dendritic cells for said human blood sources;

(e) combining said solutions of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells from said human blood sources with a portion of said first pepset;

(f) combining said solutions of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with each of said pepsets from said additional proteins;

(g) measuring proliferation of said T-cells in steps (e) and (f), to determine the responses to each peptide in said first and at least one additional pepset;

(h) compiling the responses of the T-cells in step (g) for said first protein and said additional proteins;

(i) determining the structure value of said compiled responses of step (h) for said first protein and said additional proteins; and

(j) comparing the structure value obtained for said first protein with said structure value for said additional proteins to determine the immunogenicity ranking of said first protein and said additional proteins.

15. The method of Claim 14, wherein said pepsets comprise peptides of about 15 amino acids in length.

16. The method of Claim 15, wherein said peptides overlap each adjacent peptide by about 3 amino acids.

17. The method of Claim 14, wherein the protein having the lowest structure value is ranked as being less immunogenic than the protein having the higher structure value.

18. The method of Claim 14, wherein said protein of interest and said at least one additional protein of interest are selected from the group of proteins consisting of enzymes, antibodies, structural proteins, binding proteins, and hormones.

19. The method of Claim 18, wherein said enzyme is selected from the group consisting of proteases, subtilisins, cytokines, lipases, cellulases, amylases, oxidases, isomerases, kinases, phosphatases, lactamases, and reductases.

20. The method of Claim 14, wherein said at least one additional protein of interest comprises said protein of interest that has been modified to produce a modified protein of interest.

21. The method of Claim 14, wherein said modified protein of interest is selected from the group consisting of hypoimmunogenic proteins and hyperimmunogenic proteins.

22. The method of Claim 20, wherein said modified protein of interest is produced by substituting at least one amino acid in said at least one additional protein of interest to produce a variant protein of interest.

23. The method of Claim 14, wherein the protein having a stimulation index value of between about 2.7 and about 3.2 is considered to have a positive response.

24. The method of Claim 14, wherein the stimulation index values of said protein of interest and said at least one additional protein are compared.

25. The method of Claim 14, comprising the further step of categorizing said first protein and said second protein, based on the background percent response and the structure values obtained for each of said first and second proteins.

26. The method of Claim 14, further comprising a validation assay comprising a peripheral blood mononuclear cell response assessment.

27. A method for ranking the relative immunogenicity of two proteins, wherein the second protein is a protein variant of the first protein, comprising the following steps in operable order:

(a) preparing a first pepset from said first protein and a second pepset from said second protein;

(b) obtaining from a solution comprising dendritic cells and a solution of naïve CD4+ and/or CD8+ T-cells, wherein both of said solutions are obtained from a single blood source;

(c) differentiating said dendritic cells to produce a solution of differentiated dendritic cells;

(d) combining said solution of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with said first pepset;

(e) combining said solution of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with said second pepset;

(f) measuring proliferation of said T-cells in steps (d) and (e), to determine the responses to each peptide in the first and second pepsets;

(g) compiling the responses obtained for said T-cells in step (f) for said first protein and said second protein;

(h) determining the structure value of the compiled responses of step (g) for said first protein and said second protein;

(i) comparing said structure value obtained for said first protein with said structure value for said second protein to determine the immunogenicity ranking of said first protein and said second protein.

28. The method of Claim 27, wherein said second protein is ranked as being less immunogenic than the said first protein.

29. The method of Claim 27, wherein said first protein is ranked as being less immunogenic than the said second protein.

30. The method of Claim 27, wherein said pepsets comprise peptides of about 15 amino acids in length.

31. The method of Claim 30, wherein said peptides overlap each adjacent peptide by about 3 amino acids.

32. The method of Claim 27, wherein said first protein is selected from the group of proteins consisting of enzymes, antibodies, structural proteins, binding proteins, and hormones.

33. The method of Claim 27, wherein said enzyme is selected from the group consisting of proteases, subtilisins, cytokines, lipases, cellulases, amylases, oxidases, isomerases, kinases, phosphatases, lactamases, soluble receptors, fusion proteins, and reductases.

34. The method of Claim 27, wherein said second protein comprises a reduction of at least one prominent region in said first protein.

35. The method of Claim 27, wherein the proliferation of said T-cells in step (f) for said first protein is at background level.

36. The method of Claim 27, wherein the proliferation of said T-cells in step (f) for at least one variant protein is at a background level.

37. The method of Claim 27, further comprising a validation assay comprising a peripheral blood mononuclear cell response assessment.

38. A method for determining the immune response of a test population against a test protein, comprising the following steps in operable order:

(a) preparing a pepset from a test protein;

(b) obtaining a plurality of solutions comprising human dendritic cells and a plurality of solutions of naïve human CD4+ and/or CD8+ T-cells, wherein said solutions of human dendritic cells and solutions of naïve human CD4+ and/or CD8+ T-cells are obtained from a plurality of individuals within said test population;

(c) differentiating said dendritic cells to produce a plurality of solutions comprising differentiated dendritic cells;

(d) combining said plurality of solutions of differentiated dendritic cells and said solutions of naïve CD4+ and/or CD8+ T-cells with said pepset, wherein each of said solutions of differentiated dendritic cells and naïve CD4+ and/or CD8+ T-cells are from one individual within said test population are combined;

(e) measuring proliferation of said T-cells in step (d), to determine the responses to each peptide in said pepset;

(g) compiling the responses of said T-cells in step (e) for said test protein;

(h) determining the structure value of said compiled responses obtained in step (g) for said test protein; and

(i) determining the level of exposure of said plurality of individuals to said test protein.

39. The method of Claim 38, wherein said pepsets comprise peptides of about 15 amino acids in length.

40. The method of Claim 39, wherein said peptides overlap each adjacent peptide by about 3 amino acids.

41. The method of Claim 38, wherein said test protein is selected from the group of proteins consisting of enzymes, antibodies, soluble receptors, fusion proteins, structural proteins, binding proteins, and hormones.

42. The method of Claim 38, wherein said enzyme is selected from the group consisting of proteases, subtilisins, cytokines, lipases, cellulases, amylases, oxidases, isomerases, kinases, phosphatases, lactamases, and reductases.

43. The method of Claim 38, wherein the exposure level of said plurality of individuals to said test protein is compared.

44. The method of Claim 38, further comprising at least one additional test protein.

45. The method of Claim 44, wherein said at least one additional test protein is obtained by modifying said test protein.

46. The method of Claim 44, wherein the background percent response and structure values of said test protein and said at least one additional test protein are categorized and/or ranked.

47. The method of Claim 38, further comprising a validation assay comprising a peripheral blood mononuclear cell response assessment.